

F i g. 2

HP02612 61' KVLGGGRKPRILHRRHRYKLVEDTKHRPKENLELITQSVENVGVRGDLVSVKKSIGR
 RL9_MYCLE 1"* * * * *
 MKLILTADVDHLGSGVDTVFVKDGYGR
 HP02612 121' NLLLPQGLAVYASPENKKLFEEKLLKQEGKLEKIQTAKGEALGVVVVAPHTIKLPFEDIT
 RL9_MYCLE 28" NLLPHGLAIVASRGAQRQADEIRAR-ETKAMRDREHANEIKVAIEALGVSILPMKTVA
* * * * *
 HP02612 181' HWGEYWCETVNGLDTVRVPM5VVNFEPKPKTKRYKYWLAAQQAAMAPTSPOI
* * * * *
 RL9_MYCLE 87" DSGKLFGSVTAGDVVAAIKKAGGNLDDKRIVRLPKTHIKAVGTHPVSVVHLHPEVDVVLL

Fig. 4

HP10120 1' MQRVSGLLSWTLSRVLWLSGLSEFGAARQPRIMEE-KALEVVDLIRTIIRDPEKPNLEEL
 CEF45G2 1" MCQERLDNANFTLEDSKPRHRPVGTGERDESVEDPIDSWEIFDLIRINDPEHPYTLQOL
 HP10120 60' EWSVESCVEVQEINEEYLVIRFTPTVPHCSLATLIVGNLHF
 CEF45G2 61" NVQBELIKV-FIDEETFFVKVNFPTTIPHCSMATLIGLAIRVKLLRSLRHPKVKVSVIT

Fig. 5

HP10421 1' MAAAGLALLCRRVSSALKSSRLITPQVPACTGFFLSILPKSTPNVTSFHOYRLLLHTTYS
 B0261.4 1" MGEATVRWSALAAHLLFFGSKVFSKIFYFLMFFKSTWWSLPSIVS-SAVRSQNAVNT
 HP10421 61' R--KGLEEFFDDPKNWG---QEKVKSAAWTCQQLRNKSNEDLHKLWVVLKERNMLIT
 B0261.4 58" RFSSTMKQFFDDEANFGKAEELRPKHPGRSMTAEELRLKNSDLHKLWVVLKERNMLIT
 HP10421 115' LEQEAQRQLPMPSPERLDKVVDSDALDKVVQEREDALRLLTQGERARPGAMWRDIFG
 B0261.4 118" MKKAHTSRARNMNPRLDRVHETMDRIESVVERNDVFRLETG-ESAAPKKTITTSFA
 HP10421 175' RIITWHK-FKQWVIPWHL-NKRYNKRFFALPYVDHFLRLER---KRAIRIKARKENLERK
 B0261.4 177" GFTYQKQATEHFAPQLGQKEYETPYLDDDAVVMQKMQEKEFMKNRDLDDDEKRAART
 HP10421 230' KAKILLKPPHIAEAQKSSLV
 B0261.4 237" EDMDRFKGAPRVFNR

Fig. 6

HP10582 1' MDSNHQSNYKLSKTEKKFLRKQIKAKHTLLRHE-GIETVSYATQSLVAVANGGLGN
 YKY5_CAEEL 361" RELSYFNEEKAKRIGERFEGGKLAKVHKHSIEQLKRHPDVQISTEPTKYLLVNSSILC
 HP10582 55' GVSBNQLLPV-LEKCGLDALLMPPNKPYSFYARYRTTEESKRAYTYTLNGKEVVDLQKRI
 YKY5_CAEEL 421" GVSILEELEEIFLPLDELAERFIVYPNKRYSYFVQCSSTEKSIQVRTLHGLIPPSLKNSHQ
 HP10582 114' TLYLNFKVQVKELRPQALPPGLMVVEEIIISSEERKMLLESVDWTDETDNQNSQKSLKH
 YKY5_CAEEL 481" PFAISYVENLPEATKCEDFRPANIKIIEYVSSDLEKEIVDLV-----TNHPSVQSLKH
 HP10582 174' RRVKHFGYEFHYENNNVDKDKPLSGGLPDICSEFLKWLKGYIKHKPDQMTINQYEPGQ
 YKY5_CAEEL 535" RAVVHFGHVFDYSTNSASEWKE-ADPIPPVINSLIDRLISDKYITERPDQVTANVYESGH
 HP10582 234' GIPAHIDTHSAFEDIVSLSLGSEIVMDFKH--PDGIAPVPMPLPRSLVMTGESRYLWT
 YKY5_CAEEL 594" GIFSHYDTHSAFDDPIVSISSLSDVVMEFKDGANSARIAPVLLKARSLCIIQESRYHWK
 HP10582 292' HGITCRKFDVTQASESLKSGIITSDVGDLTLSKRGLRSTFTFRKVRQTPCNCYSPLVCDSS
 YKY5_CAEEL 654" HGIVNRKYD-----V-----DPRTRNVVPRQTRVSLTLRKIRKKECEWKEFCDW

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Fi. 6-1

[illegible]

80

HP10160	1	MASRGFTETSKLQNLKQLEKQDLRLMQQLDLECRRELDTDEYETKKEETLEQLSEFNDLSL
ZK1248	1	MGVDDLLIKNAQKTIDRLIRQLAETQENNELEDEYRELRDTYVNLQLEYGKIV
HP10160	61	KKIMSGNMTLVDELSCMQLAQAIISQAKTPEVIRFLFAKQPGQLRTRLAEMDRDLAVG
ZK1248	56	ERLQGGDVSLIDDLTAPKIALRTAPAIKSAKTFEIMALFAGKHTGLLRKLMMTETNYSQ
HP10160	121	KLERDLYTQKQVEIILTALRKLGKLTADDAEFLSAGAGAILSQFEKVSTDLGSGDKILAL
ZK1248	116	KMPKQGYLERKFEIIMALRLREETITEDERKFLSRLET--PEQLTEANANRLFSGNVT
HP10160	181	ASFEVEKTKK
ZK1248	174	SPVFRVOIMASPKPKVRLDDKTENVSPKAWWHTEKKRKFVTDNKTRESLWDHPNTR

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65.

HP10173	1'	KKLLTHNLLSSHVGVGRGFPRLRQAQTEVRLCPVEFPNPFVARNIPKVEHSAFLERADN
CC04H5	1"	KKLLTHNLLSSHVGVGRGFPRLRQAQTEVRLCPVEFPNPFVARNIPKVEHSAFLERADN
HP10173	61'	LRLIQ-VPKGPFVGVEE-NEEFIRLTHHLLLEVEIEFLQCPESGRMFPISRGIPNNMLL
CC04H5	61"	LRLIQ-VPKGPFVGVEE-NEEFIRLTHHLLLEVEIEFLQCPESGRMFPISRGIPNNMLL
HP10173	119'	SEETES
CC04H5	121"	VDAEK

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Fi. 10.

HP02644	1'	MKLDKTKSRPKQSSCGKFQTKGLIKVVGRKWEKVIDPNMFADQGGDDLVCFEELTDYQVLS
CEL#55F8	1"	MTNISIPGNWQTCUVEA---MDGDFDDNM-LQFLGSEFEVL
HP02644	61'	PAKNPSSILF SKEAPKKAQAVSEEEEEEEKSSPKKKIKLKSKNVATGTSIQKEFEV
CEL#55F8	38"	P--EGVEVETKKGAKKKKPKKVENTERPEDAKCVERRLAKLKRKEQMAANKQ---*
HP02644	121'	KDPELEAQGDIMVCDDPAGENTSINLVQAPKKNKKGKIGLEPSQSTAARKVPKKAKTW
CEL#55F8	93"	KKERL---AKRKQKEAESAKKSENATETTETTERKEQ--KKRKGENDYK--PKKSK---
HP02644	181'	IPEVHDQKADVSAWKDL-FVPRVVLRSALTGFSAPTPQALTLALIRDKLDILGAAET
CEL#55F8	145"	--KEASKTKTISAMKQFYFLPNEVLEALEQGFSEETIQSAVLPAAVRDRQDVLGAAET
HP02644	240'	GSCKTTLAFLPMIHAVLQWOKRNDAPPSNTIAPPGETRTAGATRSPGKAFAESDILP
CEL#55F8	203"	GSCKTTLAFLGIPILVARLLESDDSQFTESTEVRGPR-----*

Fig. 10-1

HP02644 300' DDTVTESEALPSDIAEERAKTGGTVSDQALLFGDDAGCGPSSILREKPVPKQNEENEFE
 CELF55F8 263" -----
 HP02644 360' NLIKQVTCENLKQELDDKSATCKAYPKRPILGLVLTPTRELAUVQVKQHIDAVARFTGIKTA
 CELF55F8 323" -----
 ***** * . . .
 -----ALIVAPTRELVIQIMKHINALISTWTQIAT
 HP02644 420' ILVGGESTQKQORML-NRRPEIIVATFGRLWELIKEKHY--HLRNLRQURCLVVDADRML
 CELF55F8 383" SIVGGLAQVKQERIISQORPDIVATFGRLWAMMQEAEETGEFTLAEWKDKLCLVVDETDRM
 ***** * . . .
 ***** * . . .
 HP02644 477' VEKGHTPAELSQLLEMLNDSQYNPKRQTLVFSATLTLVHQAPARILKKHTKMDKTAKLD
 CELF55F8 443" VEEGYTAELTHILNKIHEESEKELQTLVFSATLTFAKAQDVAAEEKKAKELSSQKQIQ
 ***** * . . .
 ***** * . . .
 HP02644 537' LLMQKIGMR-GKPKVIDLTRNEATVETLTKIHCHET-DEKDFYLYYFMQYFGRSIVFA
 CELF55F8 503' RLILKLTGLRENKHKVIDLTRQMGTAOCLVEARINCNLLEKDTSLVYLLTRYPGRTIVFV
 ***** * . . .
 ***** * . . .

Fi 2.11

[illegible]

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09/890638

Fig. 12

HP10437 1' MOKSCEENEGKQNMKAEEDRPLEDVQAEGNFQPSSEGVSQEAEGNPRGGFNQPGQG
 pp21 *****
 1" MKSCQKMEGKPN---ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIOSLQE
 HP10437 61' FKEDTPVVRHLDPPEMIRGVDELERLRREIRRVNRKFMVMHWKQRHSRSRYPVCFRP
 pp21 *****
 56" FKEDIHNRHLSNEDMFREVDI---DEIRRVNRKLIVRWKVRNHHPPYLM

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Fig. 13

HP10525 1' MELSAYLREKLQRDLAEHVEVEDTINRCSCTFVLVVSATKFGKPLLQRRHRLVNACL
 SPAC8C9 1" MVNAQQLELLIQNTLEPTHTIEIQDM-SGGCGQNFVITVSPLEFGKSTLAHRLVNHKL
 HP10525 61' AELPHIHAFEQ-KTLTPDQWARERQK
 SPAC8C9 59" QEVINDIHAFQVRTLSPRHIR

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Fig. 14

HP10543	1'	MAATPEILAAATGSPAAPVPEKLEAGGSSAPERNCGVSSLPEASPPAPPEPSPNAAVPEP	.. ** . * . . . *	MAAPQPSQDPQSPAAPPEQEGAGDCA
LEAP1	1'			
HP10543	61'	ITPTRAASAALEPLGPAVSVAPQAEARSTPGPAGSRGPETFRQFRQFQYQDAA	* * . . . * * * * * * * *	
LEAP1	28'	AFSPDSSGSPAPELGAPALNTAPYADAVLUR---	PGASRGPETFRQFRQFQYQDAA	
HP10543	121'	GPREFAPQRLRELSRQWLRPDINTREKQIVEMIVQEQLLAILPEAARLRIRRTDVIRNG	*****	
LEAP1	84'	GPREFAPQRLRELSRQWLRPDINTREKQIVEMIVQEQLLAILPEAARLRIRRTDVIRNG	*****	

Fig. 15

HP03090 1' MAARRALHFVKVGNRFQARFYRDVLGNKVL RHEEFEGCKAACNGPYDGKWSKTMVGF
 CEHYPO 1" M*ARALHYFVKVANRAKTIDFTTNVLNKKVL RHEEFEGCKEATCNGPYNGRWSKTMIGY
 HP03090 61' GPEDDHFVAELTYNYGVGDYKLGNDPMGITLASSQAVSNARKLEWPLTEVAEGVTFETAP
 CEHYPO 60" GSEDEHFVLEITYNYPIHKYELGNDYRAIVDSQLEKVEKIN--HRKSGCGRI LAVKDP
 HP03090 121' GGYKFYLQNRSLPOSDFVLKVTLAVSDLQKSLNYWCNLLGMKIVEKDEEKQORALIGYADN
 CEHYPO 118" DGHEF--KIGKADQSPKVLRVQNVGDLKSKKYNETLGMPIVEEKSRI--MSYGDG
 HP03090 181' QCKLELQGVKGGVDHAAAFGRIAFSCPQKLPDLKMKRENQKILTPVLVSLDTPGKATV
 CEHYPO 174" QCELEIVKRSQDKIDRKTGFRGIAFSYPEDKLES LQDKIKSANGTINIETLTETPGKADV
 HP03090 241' QVVILADPDGHEICFVGDEAFRELKMDPEGSKLLDDADAAADKDEWPAKHNKPKASG
 CEHYPO 234" QVVILADPDGHEICFVGDEGFRALSKIDDKAESLKEQIKKDDSEKWI

Fig. 16

HP03145 1' MLGSRAAGFARGURALALAWLPGWRGRSFALARAAAGAPHGDDIQPPACPEPRGRQLSLSA
SCCOQ2 1" MIIPFIASPARYFLRTFSWSAVAIFQAVKIKPLQLRTSNSSNVTNLLSPSK
HP03145 61' AAVVDSAPRPLQPYLRIMELDKPIGTWLLYLPCTWISGLAA---EPCCFPDWVMLSFGT
SCCOQ2 53" KSWKDLFSKRWQYAEISRAGSPGTGYLLYSFCTWSTIIMAAAYDSSLVNVTKMLALFGV
HP03145 118' GAILMRGAGCTINDMWDQDYDKKVTRTANRPITAAAGDISTFQSFVFLGGQLTLALGVLLCL
SCCOQ2 113" GSFLMRGAGCVINDLWDRELDRAKVERSKSRPLASGKLSVRQAISLLSVQLTASLGLLLQL
HP03145 178' NYVSTALGAGSLLLVITYPLMKRI SYWPLALGLTFNMGALLGWSA IKG-SC-DPSVCIP
SCCOQ2 173" NEYTTIKLGVASLVPVCIYPMKRITYYQVVLGLTFGVGAVMGWPA LAGEACNMNWSVAP
HP03145 236' LYFSGVMWFTLIYDTIYAHQDKRDDVLIGLKSTALRFGENTKPMWSGFSVAMLGALSUGV
SCCOQ2 233" LXLSTISWITVLXYDTIYAHQDKRDDVKANIYSTALRFGDNTKPVLCGLAALQIATLATAGI
HP03145 296' NSGQTAPYYA-ALGAVGAHLTHQIYTLDIHRPEDCWNRFTISNRTLGLIIVFLGIVLGNLWK
SCCOQ2 293" MNGQGPVFVTLGVAGAAAYRLSNITKYKVDLDDPKDCFRWFKRNSNTGYLVAAALALDLWLK
HP03145 355' EKKTDTKKKGIENKIEN
SCCOQ2 353" SFTYDS

[illegible]

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Fi 18

1	1'	MAICALITRALSLINLAPPTVAAPAPSLFPAAQOMNGLLQQPSALMILPCRPVLTSVALIN	
BRPL2	1"		MGLKRPKPVTPGRRFVVI
61	61'	ANFVSWKSRKTYITPVWRKSGRBDHTGRIRVHIGGGHKQHYRMIDFLRPRPEPKSG	
BRPL2	19"	SDFSIDTKTEPEKSLILAPLKTGGRNHGVRVTHRGGGKKRHYRLIDFKRY----	DKAG
121	121'	PFEKVIVQRVDPCHSADIALVA--GGSRKKWIIATENQAGDTILNSNHIGHMAVAAREG	
BRPL2	75"	-IPAKVLALEYDPNSSARIALLLYADGEKRYILAPKGVNVGDTLMSGPD--	AETRP--G
180	180'	DAHPLGALPVGTILNNVSEFPGRAQVIRAAAGAGNVHNSRPSIQR	
BRPL2	129"	NALPLEKTPVGTLVHNVFTPGKGOTARAAGVYCOLMAKEGNYALLRMPSGELRKVHIK	

F i g. 1 9

HP10648 181' LTPRAPGSPRGQHEPSKPPVAGETVTGGFGAKKRKSSSQAPASKLNKELPVIPKGP
 CEY40B1B 1"

HP10648 241' KSGRVWKDRGKRFQMLQDKPLRTSWQRKMERQERKLAQDFARHLEEKERRRQEKKQ
 CEY40B1B 15" KSNRWKTKQEKHSEIKKVKTKLSTWDKKMELKAKKDMVKRVQDNIREKQVQERQEKKE
 HP10648 301' BRAENLKRRLENERKAEVQVIRNPAKLKRAKKQLRSIEKRDPLALLQKQPPQOPPAKI
 CEY40B1B 75" RKVEQEKRLENERKAEIVQKITKIHKLKKTKRQLRSIQMRDVTQVTK

MSTGANLLVMNDTC

HP10162	1	MEPOEERETQVAWLKKIFGDHPQPQYEVNPRPTEILHLHLSERNVRURDQVJLVIEDLQK	*****
RRUNK	1	MAALEEKASQVAEWKIFGDHPQPQYEMARPTEILYHLSENRVRORDQNVJLVEDLRP	*****
HP10162	61	KASEYESAKYLQDLILMESVNFPSPANLSGTSRYLNAIVDSAVALETKDTSLASFIPAVN	*****
RRUNK	61	KASEYESAKHLEDFLESVNFPSPANLSGTSRFNAIVDSATALEIKDTSIASFIPAVN	*****
HP10162	121	DI7SDLFRTKSKSEEI KLELEKLNLTATLVLEKCIQEDVKKAELHLSTERAKVDRNRQ	*****
RRUNK	121	DI7SDLFRTKSKSEEI KLEIKLEKLNLTATLVLEKCIREDLKKADVHL5AERAKAEGRLQ	*****
HP10162	181	NMDFTLKAKESEFRFGI KAAEEQLSARGMDASLSHQSTVALSEKLKQQTPLPKKLES	*****
RRUNK	181	NMDFTLKAKESEFRFGI RAAEEQLSARGMDASLSHRSTVALSDKLSLQKQQTPLPKKLES	*****
HP10162	241	YLDLMPNPSIAQVKTEEKREIDSTEAFLTRVDMDEL	*****
RRUNK	241	YLDLMPNPSIAQVKTEEKREIDATEAFLTRVDMDEL	*****

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Fig. 21

HP10334 1' MSGLRVYSTVTSREIKSQSQSEVTRILDKRIQYQLVDISQDNALRDEM---ALAGNP
 HSH3 1" MVIRVYIASSSGSTAIKKKQDVLGFLGFEANKIGFEEKDIAAENEENRKWMRENVPENSRP
 HP10334 58' KAT---PPQIVNGDQYCGDYELFVEAVEQNTLQEFKLKLA
 HSH3 60" ATGYELPPQIFNESQYRGDYDAFFEAENNAVYAFGLGTAPFGSKAEVQAKQQA

F i g. 2 2

HP10532	1'	MAGSEELGLNEDTLRVLAAPLARGEAGSFVTPPSPAQEPTDFLSRLRCLFCSLGR
HSBBK	1"	MAGSEELGLNEDTLRVLAAPLARGEAGSFVTPPSPAQEPTDFLSRLRCLFCSLGR
HP10532	61'	GAAPSESPRCSLPIRRCYGLEEGPATPDFYALVAQRLEQLVQEQKPPSPPELQGPST
HSBBK	60"	GAAPSESPRCSLPIRRCYGLEEGPATPDFYALVAQRLEQLVQEQKPPSPPELQGPST
HP10532	121'	EKEAILRRIVALLEEEAEVINOK-----EGILAV
HSBBK	120"	EKEAILRRIVALLEEEAEVINQKIASDPALRSKLVLSSDSFARIVELFCSRDDSSRFSR
HP10532	181'	ACPGPPPPSPEPLARLALAMELSRRVAGLGTTAGLSVEHVHSFTTWIQAHGNGEILAV
HSBBK	180"	ACPGPPPPSPEPLARLALAMELSRRVAGLGTTAGLSVEHVHSFTTWIQAHGNGEILAV
HP10532	241'	SFVDNLNPLD
HSBBK	240"	SFVDNLNPLD

F i g. 2 3

HP10559	1'	MPVKKKRSPGVAAVAEDGGLKKCKISSYCRSQPPARLISGE ** .***. . * . * . * . * . * . * . * . *
K1AA	61"	QTGSLRCSGSDCFNKVMPPRKKRR-----PASGDDL\$AKKSRHDSMYRKYDSTRIKTEE * .***. . * . * . * . * . * . * . * . *
HP10559	44'	EHFSSKKCLAWFYEYAGPDEVVGPGEKFCEDIGVEPENIIMLVLAWKLEAESMGFFTK * .***. . * . * . * . * . * . * . * . *
K1AA	116"	EAFSSKRCLWFYEYAGTDDVVGPGEKFCEDIGVEPENIIMLVLAWKLDQNMGYFTL * .***. . * . * . * . * . * . * . * . *
HP10559	104'	EEMLKGMTSLQCDCTEKLQNKDFLRSQINDISSEKNIYRYAFDFARDKQSLDIDTAK * .***. . * . * . * . * . * . * . * . *
K1AA	176"	QEWLKGMTSLQCCTTEKLRTLDYLSFINSTNEKLIYRYAFDFAREKQKQSLDINTAK * .***. . * . * . * . * . * . * . * . *
HP10559	164'	SMLALLGRTPLEFSVFYQYLEQSKYRVNKKQWYNVLEFSRTVHADLSNYDEGAWPVL * .***. . * . * . * . * . * . * . * . *
K1AA	236"	CMIGLLIGKIWPLFPVPHQFLEQSKYKVINKQWCNVLEFSRTINMILSNYDEGAWPVL * .***. . * . * . * . * . * . * . * . *
HP10559	224'	LDEFVEWQKVRQHS * .***. . * . * . * . * . * . *
K1AA	296"	LDEFVEWYKDKQMS * .***. . * . * . * . * . * . *

Fig. 24

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HP10562 61' QESPEDFLKLFTDPNEVYCSAPEGSDSGISEDCHPDPSPAPRATSSPMLYEVVYEAG
LZIP      1" MELELDAGDQDLIAFLLESGDLGTPADEAVRAPLDMALPLSEVPFSDWEVDL
HP10562 121' ALERNQGETGFNVGLISIQLDQSPAFMWVDDCMVSELFPDAHAHILPRAGTVAPVPCVT
LZIP      54" LCSLLSPASINILSSNPNCLVHHHTYSIPRETVSMDLESESCRKEGTQMTFQHMEELA
HP10562 181' LLFCQTLFTDEKRLILQEGVSLPSHLPLTKAEERVLKKVRKIRNKQSAQDSRRKKE
LZIP      * ***** ** ***** ** ***** ** ***** ** ***** **
114" EQFIARLVITDEKSLLEKEGLIILPETIPLTKTEEQILKVRVRIRNKRSQAQESRRKKV
HP10562 241' YIDGLESRAACSAQNELQKVKQLELHNLSVAQLRQLQTLIAQTSNKAAQTSTCVLI
LZIP      * ***** ** ***** ** ***** ** ***** ** ***** **
174" YVGGLESRVLYTAQNMELQNKVQLLEEQNLSDLLQLRKLIQAMVIEITSNKTSSSTCILI
HP10562 301' LIFSIALIILPSFPFSR----PEAGSEDYQPHGVTSRN--ILTHKDVNTENLETQVVES
LZIP      ** ***** ** ***** ** ***** ** ***** ** ***** **
234" LNVSFCLLIVPAMYSDTRGSLPAEHGVLSRQLRALPSEDYQLELPAQSEVPKDSHTHQ
HP10562 355' RLREPPGAKDANGSTRITLLEKMGKPRPSGRIRSVLHADEM
LZIP      * ***** ** ***** ** ***** ** ***** ** ***** **
294" WLDSGXCVLQAPGNTSCLLHYMPQAFSAEPPLWFFPDLFSEPLCRGPILPLQANLTRKG

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HP10456 1' MSNMEKHLFNLKFAAKELSRSAKKCDKEEKAEEKAKIKKAIQKGNMEVARIHAEN
 CEEC-2 1" MGAGESMALEKHLFDLKFAAQLEKNAQCEKDEKVEKDKLTAAIKKGNKEVAQVHAEN
 HP10456 55' AIROKNOAVNFLRMSARVDVAARVQTAVTMGKVTKSMAGVVVKSMDATLKTMLNLEKISAL
 CEEC-2 61" AIRKKNEAVNYIKMAARIIDAVAAARVQTAATQKRVTASMSGVVVKAMESAMKSMNLEKVQQL
 HP10456 115' MDRFEHQFETLDVQTOQMEDTMSFTTTLTPQNOVDMLLQEMADEAGLDLNMELPQOQTG
 CEEC-2 121" MDRFERDFEOLDVTTTKTMEKTMDOGTTLNAPKSQVDALIAEADKAGIELNQELPSNVPT
 HP10456 175' SVGTSTV-ASAEQDELSQRLARLDQV
 CEEC-2 181" ALPTGTQAVSEDKDLTERIAALNNM

Fig. 26

HP10498 1' MATPSLRGLARFGNPRKPVLPKNKPLILANRV-GERRREKGEATCITEMSVNMA
 CEC24 1" MWFSSPLLKEKALARGKSIYPRVAVFSEILPLASKNRVQAGQKPRAASSCTQELQALFG
 * * . * . . . * * * * * * * *
 HP10498 55' CWKQNEFRDACKETIQGLDCAAR-AQEARMMR--SIQETIGESGSLIPNKLKLLQRF
 CEC24 61" CLKKWEFDVPCSKQHTLYMDCVHKGAEEAAAYRDAIRKGTIGESGAGGKQSWTSAQFNK
 * * * * * * * * * * * * * * *
 HP10498 112' PNKPFLS
 CEC24 121" IQKLEFPQDLGQPYQMKRLEPTQDYADDTFRRKHWSGKRS

[illegible]

HP10505 1' MAKHLKFTARTVMVQEGNVESAYRTLNRIILTMDGLIEDIKHRRVYEKPCRRRQRESYERC

CEF29 1" MVONNDVDGAFGLLNRLMDSEGMLKITRRTQFYQKPYMQRK'TLSMEAS

HP10505 61' RRIYNNMEMARKINFILMRKNRADPWQGC

49" TAI FNE DMNR KMKFLVRKNRPDKHPGGVTS

HP10515 1' MFLPAL-LWGRPLPGHQWLGKRRPRVSLRAQNNMIRRLTEAKENHYWLSWPMYMTREQL
DM63B 1" MHLTLINLFKKTYPGHI FGKRRLLVKSQSRAMDTLTREYERQEQVMLLLRHP YLTMEQS
HP10515 60' RGAH-AVRREAFEA-IKAAATSKFPHPHFADQLDLNLVNTKWS
DM63B 61" FGHAKELQKREKIVARWTDGT/LKMKPHVYTFIERLNQLKKEAMD

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Fig. 29

HP01124 1' MGTKESEFEDCKQKQFQAASVSIQNLPKNGSYRPSYEMLRFVSYKYQATMGPCIVRRPQ
 H9ACBP 1' MSQAEPFKAAEVRHL----KTKPSDEMLFTYGHYKQATVGCDINTERPG
 HP01124 60' FWDPTGRYKWDANNSLKGKMSREAMSAYITENKIVAQITDTPVLEGAEDMFGFYEPFLY
 H9ACBP 47' MLDFTGKAKVDANWELKGYSKEDAMKAYINVEVSLKKYGI

[illegible]

HP10101	1'	MTAKVSEERSGRRHRDGDVLT.PAGVVVKQERLSPVAPAHRRPDHSGGSPPTSE
HP10101	60'	ARGSHGNRARGVSRSPFKKKNKASGRBSKSPRSKNNRSPHHSTVVKQEREDHPRGRE
CEC32E8	1'	MGDRSDRRHRDRSPERRRRSRKSRDRQ*RRD-T
HP10101	121'	DQHRPEQEQRHRRARNRDRHRGHSRQRTSNRPSGQGGQGRDRDTQNLQAQEEERE
CEC32E8	36"	RDDSPKTKREVKEEQSDNSPRRRDRDGGRRDRDRDRNRDRD-RDHRDRDGRDRDRD
HP10101	181'	FYNARRRHRQRNDVGGGSESELVPRPGNNKEKEVPAKEKSPFELSGALLEDTNTFR
CEC32E8	95"	NF--RRPDVPRVEDKQYGLKTEENWGKPEPAKEK-----EKVNLGTSGALTEDTNTFR
HP10101	241'	GVVIKYSEPPPEARIPKRWMLYFPKNDEVLPVWYIHRQSAVILGRHRTIADIPIDHPSCS
CEC32E8	148"	GVVIKYNEPPPAKNARWLYPFGKEESLQVLYIHRQSAVILGRDHKIADIPVDHPSCS
HP10101	301'	KQHAVQYRLVVEYPRADGTGVRVQKPYIIDGSGNGVFLANKRAIEPQRYTELKEDVLKF
CEC32E8	208"	KQHAVT.QPFSMPFRDQGT*ARRIMPYIIDGSGNGVFLNEKKIEPQRYIELQEKMLKF
HP10101	361'	GFPSREYVILLHESSTYSITSEIKDKDDEDEEEEREVSUS
CEC32E8	268"	GFSTRYVVMKEREETTELAEAGDEGVKKESD

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HP10370 1' MEYDEKLARQAHINPFRKQSGFRQIEQGPGEVFDVTFEALPELPRQEPFRF
DMCG115 1" MSHWKDSITSTPGVQAQLINESASNLHASTTIGSTVGLGGSGTGGSGEAGSEESGPQ
HP10370 55' RCPERVMDLGLSEDFRBPVGLFTASDVQQLRQATECKQVILELPEQBEKQDAVVRLI
DMCG115 61" QASYRALLIPASIVREQWRLFTSTSDANTQDLQAAIANDLDVLVLEELSEERWIVRNLV
HP10370 115' HRLKLQELKDPNE-----DEPHIVLLEHNF-----YKEKSXVKQTCDK
DMCG115 121" DLAYSILQELEAQEQHLSLSSDMVMNATRAVVGHIFVPHPHHGGKRNRLQAAAKNNYCDH
HP10370 156' CNTTIWGLIQWTYTCGYRCHSKCNILISKPCVSSKVHQAUEYELNICTPETGLDHQDY
DMCG115 181" CTYTIWVVQNSVYCDGQFTVQKCIDGVKVCANHIVSBERQHPISETCPEIGLASQGY
HP10370 216' RCAECRAPFISLRGVTEARQCDYTGQYCSHCNNDLAVTPARVVHNVDFEPRKVSRCSM
DMCG115 241" KCAECOTMLATKNTWTEPRLCDYSGLYCPRCNMNDGNFIPARITIHNDFHPRRVBTAL
HP10370 276' RYALWGRPVLRRETNPLFFSVBELVEIHKLRQDILLMKPYFTTCREAMEARLL-LQ
DMCG115 301" QETBLFINKPLIILEEDNPKLFVFEVKLCVVKLQRQNVIMRHYLAACKIASBLKLVQDQ
HP10370 335' LQDRHFVDEMEYSVQDLDDVHAGLGCSTETHTLFAKHKLDCERCQAKGFWCELCR
DMCG115 361" LGVRHHLAQSEFYHISDLQSVEGALSEFLQGVFKAFNDHIR--BCPMLCAQAYICICH
HP10370 395' EGVLPFPDSDHITSVACDSAVFHRDCYTDNSTTFCRKANLSLKKQLSFQEPGPDVEA
DMCG115 420" NNEVTFPPDDGCIKQCNSTFHVAVCIATRKNNICPKCTRQENHLQLDHNKSTEDDDDD

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HP10516	1'	MAGTGLLAIRLTGPGSWVRGSGPSVLSRLQDAAVVRPGFLSWAREETLSRELEPELRRRR	DMCG141	1"	MRITTFDISEPEEQQLHEEIEPYMSRLR	HP10516	61'	YEYDHWDAATHGPRETEKSRWSEASNAILQRVQAAGFGQTLSSVHVLDLEARGYIKP	DMCG141	29"	YFDFHWDDATHGPRETEKRWKPKNREILERVQVAF--DGAVMYPVHILDIA PDGVTKP	HP10516	121'	HVDSIKFCGATIAGLSLLSPSVMLVHH--	DMCG141	87"	HVDSTRYCGNTIGISLLSDSVMLRVLTDEQRYQQSSGTATDPSQSGSEPDAAVYRHQPE	HP10516	153'	EWL-----ELLPEGSLYILGSRARYDFSHEILRDEESFFGERRIPGRRRISVTCISLP	DMCG141	147'	ASLKNFVADILLPRSLYIMGTHARYKFTHEILAKESOFQGAIVPPTRAISITICRNP
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Fig. 35

HP10580	1'		MKKFFQEFKADIKPK
			**
DMG546	61"	TLRKVLIVLLGTCVLGYSWSIYGVKVI	TERFVRPSTLKEIEELKLSKAAAFKIALTGS
HP10580	16'	SAGPGQKLKESVGEKAHKEPNQ--	PAPRPPRQGP
		NEAQMAAAAAA	LARLEQKQSRWGP
		..**....	..**....
DMG546	121"	GMGTGHLKNSPKQETPSSSRQKYAYVP	PKRNEISNEARAAASAA
			LARIDKKTSEFN-
HP10580	74'	TSQPTIRNQVRKELQAKATVSGSP-	EAPGTNVVSEPREGSA-
		HLAVPGVYFTCPL-TGA	
		**	**
DMG546	180"	TSLSAVKAQAKRELEAERRQREAMGTP	STSTSTASGGPTRNLACEGVFFRCPLISEE
HP10580	131'	TLRKQORDACIKEAIIHFSTDPVAAS	IMKIYTFNKQDQDRVKLGVDTFIAKYL
		NIHLHPE	
		..**....	..**....
DMG546	240"	ILPKSVVKVRIKEFLYQQL	EADRGLTACLIHHNCN-VKEKADECIA
			TLIRYLENLIXNPE
HP10580	191'	EEKYRKIKLQNKVFQERINCLEGTHE	FFEAIGFQKVLLPAQDQEDPEEFV
		SETTLAQP	
		..***.***.***.***.***.	***.***.***.***.***.***.
DMG546	299"	EEKFKIRMSNKKIFSEKRVYVEGAL	DVLQAAGFNEV-----QIDGEP
			LLTWREQEKD

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Fig. 35-1

HP10580 251' QSLERHKEQLLAAEFVRAKLDQRORVFQPSPLASQFELPGDFFNLTAEETKREQLRSEA
 * * * * *
 DMC546 353' LDLPTLVEALKSSEIIPIELDRNIKVLLPSQ-ACRVALPDEFYRLSPEETKKEQQLRSEA
 * * * * *
 HP10580 311' VERLSVLRTKAMREKEEQRLKTKYNTLLRVRLPDGCLLQGTFYARERLGAUVGVFVREAL
 * * * * *
 DMC546 412' IAQSQMLRTKAMREREQRLRMRYALVRVKFPNGLFIQGTENVYEKISDVFEFVQSCIL
 * * * * *
 HP10580 371' QSDWLPFELLASGGQKLSEDE-NLALNECGLVPSALLTF SWDMAVLEDIKAAGAEPSIL
 * * * * *
 DMC546 472' ADESLDFSLVNSDGLGDEDELEKTYDCKLIPTNTLLFSANDTPAPLQTDINYLKEDLL
 * * * * *
 HP10580 430' KPELLSAIEKLL
 DMC546 532' MLVQAM